

FrameAlign of: DD0017Rsid62 check: 2905 from: 1 to: 1638

Genomic DNA from 3DT corresponding to p0016.ctsas50r, US 10/744,572

to: DD0017sid8 check: 2251 from: 1 to: 237

SEQ ID NO: 8 is encoded by FIS sequence of p0016.ctsas50r

Scoring matrix: blosum62.cmp

CompCheck: 1102

BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA 89: 10915-10919.

Translation table: transl_table_01.txt transl_table = 1

This file contains the Standard Code specified in the feature table definition, Version 1.08, formatted for use with the GCG programs (Data Files volume of the Data Reference Set). It names amino acids in both one and three-letter form and lists the codons which should translate into them. All GCG translation programs may generate their .

..

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248
Frameshift Weight:	0		

Quality:	928	Length:	865
Ratio:	3.916	Gaps:	1
Percent Similarity:	99.578	Percent Identity:	99.578

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

DD0017Rsid62 x BB1410sid8 July 2, 2007 15:28 ..

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      .      .      .      .
50 atggcggccaatgcgggcggtggagcgggaggaggcagcggcagcgg 99
   ||||||||||||||||||||||||||||||||||||||||||||
  1 MetAlaAlaAsnAlaGlyGlyGlyGlyAlaGlyGlyGlySerGlySerGl 17
      .      .      .      .
100 cagcgtggctgcgccggcggtgtgccgccccagcggctcgcggtggacgc 149
   ||||||||||||||||||||||||||||||||||||||||||||
 18 ySerValAlaAlaProAlaValCysArgProSerGlySerArgTrpThrP 34
      .      .      .      .
150 cgacgccgggagcagatcaggatgctgaaggagctctactacggctgcggc 199
   ||||||||||||||||||||||||||||||||||||||||||||
 35 roThrProGluGlnIleArgMetLeuLysGluLeuTyrTyrGlyCysGly 50
      .      .      .      .
200 atccggtgcgccagctcggagcagatccagcgcaccccgccatgctgcg 249
   ||||||||||||||||||||||||||||||||||||||||||||
 51 IleArgSerProSerSerGluGlnIleGlnArgIleThrAlaMetLeuAr 67
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250 gcagcacggcaagatcgagggcaagaacgtcttctactgggtccagaacc 299
   ||||||||||||||||||||||||||||||||||||||||||||||||
68 gGlnHisGlyLysIleGluGlyLysAsnValPheTyrTrpPheGlnAsnH 84
   .
300 acaaggcccgcgagcgccagaagcgccgcctcaccagcctcgacgtcaac 349
   ||||||||||||||||||||||||||||||||||||||||||||||||
85 isLysAlaArgGluArgGlnLysArgArgLeuThrSerLeuAspValAsn 100
   .
350 gtgcccgcgcgcggcgccgacgccaccaccagccaactcggcgctcct 399
   ||||||||||||||||||||||||||||||||||||||||||||||||
101 ValProAlaAlaGlyAlaAlaAspAlaThrThrSerGlnLeuGlyValLe 117
   .
400 ctgctgtcgtcgccgcgccttcaggtacgtgctgcgtcagtgctgtggtg 449
   ||||||||||||||||||
118 uSerLeuSerSerProProPro..... 124
   .
   .
   .
550 ctgatgtgcaccgtcgtcatcactgatcaggcgcgggcgccctccctcgccc 599
   ||||||||||||||||||
125 .....SerGlyAlaAlaProProSerPro 132
   .
600 accctcggcttctacgccgcccggcaatggcgggcgatcggctgtgctgct 649
   ||||||||||||||||||
133 ThrLeuGlyPheTyrAlaAlaGlyAsnGlyGlyGlySerAlaValLeuLe 149
   .
650 ggacacgagttccgactggggcagcagcggcgctgcatggccaccgaga 699
   ||||||||||||||||||
150 uAspThrSerSerAspTrpGlySerSerGlyAlaAlaMetAlaThrGluT 166
   .
700 catgcttcctgcaggtcgggtgctgtagtacgttcttttcttgggcattgc 749
   ||||||||||||||||||
167 hrCysPheLeuGlnValGlyAlaValValArgSerPheLeuGlyHisCys 182
   .
750 ggcgagtttcacgttcgtacgtacgagttgatcgccgcgtcgttccatcc 799
   ||||||||||||||||||
183 AlaGlnPheHisValArgThrTyrGluLeuIleAlaAlaSerPheHisPr 199
   .
800 accggtatatataactgttaggtacggcggtgcgcgcccgaggactaca 849
   ||||||||||||||||||
200 oProValTyrIleThrValArgTyrGlyGlyAlaArgProGlnAspTyrM 216
   .
850 tgggcgtgacggacacgggcagctcgtcgagtgccacgcttctcgtcg 899
   ||||||||||||||||||.....|||
217 etGlyValThrAspThrGlySerSerSerGlnTrpProArgPheAlaSer 232
   .
900 tcggacacgataatg 914
   |||||||||||||||
233 SerAspThrIleMet 237

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FrameAlign of: DD0017Rsid62 check: 2905 from: 1 to: 1638

Genomic DNA from 3DT corresponding to p0016.ctsas50r, US 10/744,572

to: DD0017sid6 check: 2251 from: 1 to: 237

SEQ ID NO: 6 is encoded by EST sequence of p0016.ctsas50r

Scoring matrix: blosum62.cmp

CompCheck: 1102

BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA 89: 10915-10919.

Translation table: transl_table_01.txt transl_table = 1

This file contains the Standard Code specified in the feature table definition, Version 1.08, formatted for use with the GCG programs (Data Files volume of the Data Reference Set). It names amino acids in both one and three-letter form and lists the codons which should translate into them. All GCG translation programs may generate their .

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Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248
Frameshift Weight:	0		

Quality:	929	Length:	868
Ratio:	3.903	Gaps:	1
Percent Similarity:	99.580	Percent Identity:	99.580

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	2
.	=	1

DD0017Rsid62 x BB1410SID6 August 5, 2007 14:09 ..

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      .           .           .           .           .
50 atggcggccaatgcggggcggcggtggagcgggaggaggcagcggcagcgg 99
   |||||||||||||||||||||||||||||||||||||||||||||||||
  1 MetAlaAlaAsnAlaGlyGlyGlyGlyAlaGlyGlyGlySerGlySerGl 17

      .           .           .           .           .
100 cagcgtggctgcgccggcggtgtgccgccccagcggctcgcggtggacgc 149
   |||||||||||||||||||||||||||||||||||||||||||||||||
  18 ySerValAlaAlaProAlaValCysArgProSerGlySerArgTrpThrP 34

      .           .           .           .           .
150 cgacgccgggagcagatcaggatgctgaaggagctctactacggctgcggc 199
   |||||||||||||||||||||||||||||||||||||||||||||||||
  35 roThrProGluGlnIleArgMetLeuLysGluLeuTyrTyrGlyCysGly 50

      .           .           .           .           .
200 atccggtgcgccagctcgggagcagatccagcgcacaccgccatgctgcg 249
   |||||||||||||||||||||||||||||||||||||||||||||||||

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51  IleArgSerProSerSerGluGlnIleGlnArgIleThrAlaMetLeuAr 67

250  gcagcacggcaagatcgagggcaagaacgtcttctactggttccagaacc 299
    ||||||||||||||||||||||||||||||||||||||||||||||||
68  gGlnHisGlyLysIleGluGlyLysAsnValPheTyrTrpPheGlnAsnH 84

300  acaaggcccgcgagcgccagaagcgccgcctcaccagcctcgacgtcaac 349
    ||||||||||||||||||||||||||||||||||||||||||||||||
85  isLysAlaArgGluArgGlnLysArgArgLeuThrSerLeuAspValAsn 100

350  gtgcccgcgcgcccggcgccgacgccaccaccagccaactcggcgctcct 399
    ||||||||||||||||||||||||||||||||||||||||||||||||
101  ValProAlaAlaGlyAlaAlaAspAlaThrThrSerGlnLeuGlyValLe 117

400  ctgctgtcgtcgccgcccgccttcaggtacgtgcgctcagtgcggtgtgtg 449
    ||||||||||||||||||||
118  uSerLeuSerSerProProPro..... 124
      .
      .
      .

550  ctgatgtgcaccgtcgatcatcactgatcaggcgcgccgctccctcgccc 599
      ||||||||||||||||||||||||
125  .....SerGlyAlaAlaProProSerPro 132

600  accctcggcttctacgccgcccgaatggcgccgatcggctgtgctgct 649
    ||||||||  ||||||||||||||||||||||||||||||||||||
133  ThrLeuGlyLeuTyrAlaAlaGlyAsnGlyGlyGlySerAlaValLeuLe 149

650  ggacacgagttccgactggggcagcagcgccgctgccatggccaccgaga 699
    ||||||||||||||||||||||||||||||||||||||||||||||||
150  uAspThrSerSerAspTrpGlySerSerGlyAlaAlaMetAlaThrGluT 166

700  catgcttcctgcagggtcgggtgctgtagtacgttcttttcttgggcattgc 749
    ||||||||||||||||||||||||||||||||||||||||||||||||
167  hrCysPheLeuGlnValGlyAlaValValArgSerPheLeuGlyHisCys 182

750  ggcgcagtttcacgttcgtacgtacgagttgatcgccgcgtcgttccatcc 799
    ||||||||||||||||||||||||||||||||||||||||||||||||
183  AlaGlnPheHisValArgThrTyrGluLeuIleAlaAlaSerPheHisPr 199

800  accggtatatataactgttaggtacggcggtgcgcgcccgcaggactaca 849
    ||||||||||||||||||||||||||||||||||||||||||||||||
200  oProValTyrIleThrValArgTyrGlyGlyAlaArgProGlnAspTyrM 216

850  tgggcgtgacggacacgggcagctcgtcgagtgccacgcttctcgtcg 899
    ||||||||||||||||||||||||||||||||||||||||||||||||
217  etGlyValThrAspThrGlySerSerSerGlnTrpProArgPheSerSer 232

900  tcggacacgataatggcg 917
    ||||||||
233  SerAspThrIleMetAla 238

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